

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 09/943,857A
Source: FW/6
Date Processed by STIC: 2-25-05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 02/25/2005

PATENT APPLICATION: US/09/943,857A

TIME: 14:43:30

Input Set : A:\08919-066001.TXT

Output Set: N:\CRF4\02252005\I943857A.raw

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4 <110> APPLICANT: Shaw, Jei-Fu
5      Lee, Guan-Chiun
6      Tang, Shye-Jye
9 <120> TITLE OF INVENTION: RECOMBINANT CANDIDA RUGOSA LIPASES
12 <130> FILE REFERENCE: 08919-066001
14 <140> CURRENT APPLICATION NUMBER: US 09/943,857A
15 <141> CURRENT FILING DATE: 2001-08-31
17 <160> NUMBER OF SEQ ID NOS: 11
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1641
23 <212> TYPE: DNA
24 <213> ORGANISM: Candida rugosa
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)...(1641)
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32 Ser Met Asn Ser Arg Gly Pro Ala Gly Arg Leu Gly Ser Val Pro Thr
33 1          5          10          15
35 gcc acg ctc gcc aac ggc gac acc atc acc ggt ctc aac gcc att gtc      96
36 Ala Thr Leu Ala Asn Gly Asp Thr Ile Thr Gly Leu Asn Ala Ile Val
37          20          25          30
39 aac gaa aag ttt ctc ggc ata ccg ttt gcc gag ccg ccc gtg ggc agc      144
40 Asn Glu Lys Phe Leu Gly Ile Pro Phe Ala Glu Pro Pro Val Gly Ser
41          35          40          45
43 ctc cgc ttc aag ccg ccc gtg ccg tac tcg gcg tcg ctc aac ggc cag      192
44 Leu Arg Phe Lys Pro Pro Val Pro Tyr Ser Ala Ser Leu Asn Gly Gln
45          50          55          60
47 cag ttt acc tct tac ggc ccg tct tgc atg cag atg aac cct atg ggc      240
48 Gln Phe Thr Ser Tyr Gly Pro Ser Cys Met Gln Met Asn Pro Met Gly
49 65          70          75          80
51 tcg ttt gag gac aca ctt ccc aag aat gcg ctt gac ttg gtg ctc cag      288
52 Ser Phe Glu Asp Thr Leu Pro Lys Asn Ala Leu Asp Leu Val Leu Gln
53          85          90          95
55 tcc aag atc ttc caa gtg gtg ctt ccc aac gac gag gac tgt ctc acc      336
56 Ser Lys Ile Phe Gln Val Val Leu Pro Asn Asp Glu Asp Cys Leu Thr
57          100          105          110
59 atc aac gtg atc cgg ccg ccc ggc acc agg gcc agt gct ggt ctc ccg      384
60 Ile Asn Val Ile Arg Pro Pro Gly Thr Arg Ala Ser Ala Gly Leu Pro
61          115          120          125
63 gtg atg ctc tgg atc ttt ggc ggt ggg ttt gag ctt ggc ggc tcc agc      432
64 Val Met Leu Trp Ile Phe Gly Gly Gly Phe Glu Leu Gly Gly Ser Ser

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65	130	135	140	
67	ctc ttt cca gga gac cag atg gtg gcc aag agc gtg ctc atg ggt aaa	480		
68	Leu Phe Pro Gly Asp Gln Met Val Ala Lys Ser Val Leu Met Gly Lys			
69	145 150 155 160			
71	ccg gtg atc cac gtg agc atg aac tac cgc gtg gcg tca tgg ggg ttc	528		
72	Pro Val Ile His Val Ser Met Asn Tyr Arg Val Ala Ser Trp Gly Phe			
73	165 170 175			
75	ttg gcc ggc ccc gac atc cag aac gaa ggc agc ggg aac gcc ggc ttg	576		
76	Leu Ala Gly Pro Asp Ile Gln Asn Glu Gly Ser Gly Asn Ala Gly Leu			
77	180 185 190			
79	cat gac cag cgc ttg gcc atg cag tgg gtg gcg gac aac att gct ggg	624		
80	His Asp Gln Arg Leu Ala Met Gln Trp Val Ala Asp Asn Ile Ala Gly			
81	195 200 205			
83	ttt ggc ggc gac ccg agc aag gtg acc ata tac ggc gag tct gcg ggc	672		
84	Phe Gly Gly Asp Pro Ser Lys Val Thr Ile Tyr Gly Glu Ser Ala Gly			
85	210 215 220			
87	agc atg tcg acg ttt gtg cac ctt gtg tgg aac ggc gac aac acg	720		
88	Ser Met Ser Thr Phe Val His Leu Val Trp Asn Asp Gly Asp Asn Thr			
89	225 230 235 240			
91	tac aac ggc aag ccg ttg ttc cgc gcc gcc atc atg cag tct ggc tgc	768		
92	Tyr Asn Gly Lys Pro Leu Phe Arg Ala Ala Ile Met Gln Ser Gly Cys			
93	245 250 255			
95	atg gtg ccg tct gac ccg gtg gac ggc acg tac ggc acc gag atc tac	816		
96	Met Val Pro Ser Asp Pro Val Asp Gly Thr Tyr Gly Thr Glu Ile Tyr			
97	260 265 270			
99	aac cag gtg gtg gcg tct gcc ggg tgt ggc agt gcc agc gac aag ctc	864		
100	Asn Gln Val Val Ala Ser Ala Gly Cys Gly Ser Ala Ser Asp Lys Leu			
101	275 280 285			
103	gcg tgc ttg cgc ggc ctt tct cag gac acg ttg tac cag gcc acg agc	912		
104	Ala Cys Leu Arg Gly Leu Ser Gln Asp Thr Leu Tyr Gln Ala Thr Ser			
105	290 295 300			
107	gac acg ccc ggc gtg ttg gcg tac ccg tcg ttg cgg ttg tct tat ctc	960		
108	Asp Thr Pro Gly Val Leu Ala Tyr Pro Ser Leu Arg Leu Ser Tyr Leu			
109	305 310 315 320			
111	ccg cgg ccc gac ggc acc ttc atc acc gac gac atg tat gcc ttg gtg	1008		
112	Pro Arg Pro Asp Gly Thr Phe Ile Thr Asp Asp Met Tyr Ala Leu Val			
113	325 330 335			
115	cgg gac ggc aag tac gca cac gtg ccg gtg atc atc ggc gac cag aac	1056		
116	Arg Asp Gly Lys Tyr Ala His Val Pro Val Ile Ile Gly Asp Gln Asn			
117	340 345 350			
119	gac gag ggc act ttg ttt ggg ctc tct tct ttg aac gtg acc aca gat	1104		
120	Asp Glu Gly Thr Leu Phe Gly Leu Ser Ser Leu Asn Val Thr Thr Asp			
121	355 360 365			
123	gct cag gca cgg gcg tac ttc aag cag tct ttc atc cac gcc agc gat	1152		
124	Ala Gln Ala Arg Ala Tyr Phe Lys Gln Ser Phe Ile His Ala Ser Asp			
125	370 375 380			
127	gcg gag atc gac acg ttg atg gcg gcg tac acc agc gac atc acc cag	1200		
128	Ala Glu Ile Asp Thr Leu Met Ala Ala Tyr Thr Ser Asp Ile Thr Gln			
129	385 390 395 400			

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131 ggt tct ccg ttc gac acc ggc atc ttc aat gcc atc acc ccg cag ttc      1248
132 Gly Ser Pro Phe Asp Thr Gly Ile Phe Asn Ala Ile Thr Pro Gln Phe
133           405           410           415
135 aaa cgg atc tct gcg ttg ctt ggc gac ctt gcg ttc acg ctt gcg cgt      1296
136 Lys Arg Ile Ser Ala Leu Leu Gly Asp Leu Ala Phe Thr Leu Ala Arg
137           420           425           430
139 cgc tac ttc ctc aac tac tac cag ggc ggc acc aag tac tcg ttc ctc      1344
140 Arg Tyr Phe Leu Asn Tyr Tyr Gln Gly Gly Thr Lys Tyr Ser Phe Leu
141           435           440           445
143 tct aag cag ctt tct ggg ttg ccc gtc ttg ggc acc ttc cac ggc aac      1392
144 Ser Lys Gln Leu Ser Gly Leu Pro Val Leu Gly Thr Phe His Gly Asn
145           450           455           460
147 gac atc atc tgg cag gac tac ttg gtg ggc agc ggc agt gtg atc tac      1440
148 Asp Ile Ile Trp Gln Asp Tyr Leu Val Gly Ser Gly Ser Val Ile Tyr
149 465           470           475           480
151 aac aac gcg ttc att gcg ttt gcc aac gac ctc gac ccg aac aag gcg      1488
152 Asn Asn Ala Phe Ile Ala Phe Ala Asn Asp Leu Asp Pro Asn Lys Ala
153           485           490           495
155 ggc ttg tgg acc aac tgg ccc acg tac acc agc agc tct cag tct ggc      1536
156 Gly Leu Trp Thr Asn Trp Pro Thr Tyr Thr Ser Ser Ser Gln Ser Gly
157           500           505           510
159 aac aac ttg atg cag atc aac ggc ttg ggg ttg tac acc ggc aag gac      1584
160 Asn Asn Leu Met Gln Ile Asn Gly Leu Gly Leu Tyr Thr Gly Lys Asp
161           515           520           525
163 aac ttc cgc ccg gat gcg tac agc gcc ctc ttt tcc aac ccg ccg tct      1632
164 Asn Phe Arg Pro Asp Ala Tyr Ser Ala Leu Phe Ser Asn Pro Pro Ser
165           530           535           540
167 ttc ttt gtg      1641
168 Phe Phe Val
169 545
172 <210> SEQ ID NO: 2
173 <211> LENGTH: 547
174 <212> TYPE: PRT
175 <213> ORGANISM: Candida rugosa
177 <400> SEQUENCE: 2
178 Ser Met Asn Ser Arg Gly Pro Ala Gly Arg Leu Gly Ser Val Pro Thr
179 1           5           10           15
180 Ala Thr Leu Ala Asn Gly Asp Thr Ile Thr Gly Leu Asn Ala Ile Val
181           20           25           30
182 Asn Glu Lys Phe Leu Gly Ile Pro Phe Ala Glu Pro Pro Val Gly Ser
183           35           40           45
184 Leu Arg Phe Lys Pro Pro Val Pro Tyr Ser Ala Ser Leu Asn Gly Gln
185           50           55           60
186 Gln Phe Thr Ser Tyr Gly Pro Ser Cys Met Gln Met Asn Pro Met Gly
187 65           70           75           80
188 Ser Phe Glu Asp Thr Leu Pro Lys Asn Ala Leu Asp Leu Val Leu Gln
189           85           90           95
190 Ser Lys Ile Phe Gln Val Val Leu Pro Asn Asp Glu Asp Cys Leu Thr
191           100          105          110

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192 Ile Asn Val Ile Arg Pro Pro Gly Thr Arg Ala Ser Ala Gly Leu Pro
193      115      120      125
194 Val Met Leu Trp Ile Phe Gly Gly Gly Phe Glu Leu Gly Gly Ser Ser
195      130      135      140
196 Leu Phe Pro Gly Asp Gln Met Val Ala Lys Ser Val Leu Met Gly Lys
197 145      150      155      160
198 Pro Val Ile His Val Ser Met Asn Tyr Arg Val Ala Ser Trp Gly Phe
199      165      170      175
200 Leu Ala Gly Pro Asp Ile Gln Asn Glu Gly Ser Gly Asn Ala Gly Leu
201      180      185      190
202 His Asp Gln Arg Leu Ala Met Gln Trp Val Ala Asp Asn Ile Ala Gly
203      195      200      205
204 Phe Gly Gly Asp Pro Ser Lys Val Thr Ile Tyr Gly Glu Ser Ala Gly
205      210      215      220
206 Ser Met Ser Thr Phe Val His Leu Val Trp Asn Asp Gly Asp Asn Thr
207 225      230      235      240
208 Tyr Asn Gly Lys Pro Leu Phe Arg Ala Ala Ile Met Gln Ser Gly Cys
209      245      250      255
210 Met Val Pro Ser Asp Pro Val Asp Gly Thr Tyr Gly Thr Glu Ile Tyr
211      260      265      270
212 Asn Gln Val Val Ala Ser Ala Gly Cys Gly Ser Ala Ser Asp Lys Leu
213      275      280      285
214 Ala Cys Leu Arg Gly Leu Ser Gln Asp Thr Leu Tyr Gln Ala Thr Ser
215      290      295      300
216 Asp Thr Pro Gly Val Leu Ala Tyr Pro Ser Leu Arg Leu Ser Tyr Leu
217 305      310      315      320
218 Pro Arg Pro Asp Gly Thr Phe Ile Thr Asp Asp Met Tyr Ala Leu Val
219      325      330      335
220 Arg Asp Gly Lys Tyr Ala His Val Pro Val Ile Ile Gly Asp Gln Asn
221      340      345      350
222 Asp Glu Gly Thr Leu Phe Gly Leu Ser Ser Leu Asn Val Thr Thr Asp
223      355      360      365
224 Ala Gln Ala Arg Ala Tyr Phe Lys Gln Ser Phe Ile His Ala Ser Asp
225      370      375      380
226 Ala Glu Ile Asp Thr Leu Met Ala Ala Tyr Thr Ser Asp Ile Thr Gln
227 385      390      395      400
228 Gly Ser Pro Phe Asp Thr Gly Ile Phe Asn Ala Ile Thr Pro Gln Phe
229      405      410      415
230 Lys Arg Ile Ser Ala Leu Leu Gly Asp Leu Ala Phe Thr Leu Ala Arg
231      420      425      430
232 Arg Tyr Phe Leu Asn Tyr Tyr Gln Gly Gly Thr Lys Tyr Ser Phe Leu
233      435      440      445
234 Ser Lys Gln Leu Ser Gly Leu Pro Val Leu Gly Thr Phe His Gly Asn
235      450      455      460
236 Asp Ile Ile Trp Gln Asp Tyr Leu Val Gly Ser Gly Ser Val Ile Tyr
237 465      470      475      480
238 Asn Asn Ala Phe Ile Ala Phe Ala Asn Asp Leu Asp Pro Asn Lys Ala
239      485      490      495
240 Gly Leu Trp Thr Asn Trp Pro Thr Tyr Thr Ser Ser Ser Gln Ser Gly

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241          500          505          510
242 Asn Asn Leu Met Gln Ile Asn Gly Leu Gly Leu Tyr Thr Gly Lys Asp
243          515          520          525
244 Asn Phe Arg Pro Asp Ala Tyr Ser Ala Leu Phe Ser Asn Pro Pro Ser
245          530          535          540
246 Phe Phe Val
247 545
249 <210> SEQ ID NO: 3
250 <211> LENGTH: 1641
251 <212> TYPE: DNA
252 <213> ORGANISM: Candida rugosa
254 <220> FEATURE:
255 <221> NAME/KEY: CDS
256 <222> LOCATION: (1)...(1641)
258 <400> SEQUENCE: 3
259 tcg atg aat tca cgt ggc cca gcc ggc cgt ctc gga tcg gta ccc acc      48
260 Ser Met Asn Ser Arg Gly Pro Ala Gly Arg Leu Gly Ser Val Pro Thr
261 1          5          10          15
263 gcc aag ctc gcc aac ggc gac acc atc acc ggt ctc aac gcc atc atc      96
264 Ala Lys Leu Ala Asn Gly Asp Thr Ile Thr Gly Leu Asn Ala Ile Ile
265          20          25          30
267 aac gag gcg ttc ctc ggc att ccc ttt gcc gag ccg ccg gtg ggc aac      144
268 Asn Glu Ala Phe Leu Gly Ile Pro Phe Ala Glu Pro Pro Val Gly Asn
269          35          40          45
271 ctc cgc ttc aag gac cct gtg ccg tac tct ggc tcg ctc aac ggc cag      192
272 Leu Arg Phe Lys Asp Pro Val Pro Tyr Ser Gly Ser Leu Asn Gly Gln
273          50          55          60
275 aag ttc act tct tac ggc ccg tct tgc atg cag cag aac ccc gag ggc      240
276 Lys Phe Thr Ser Tyr Gly Pro Ser Cys Met Gln Gln Asn Pro Glu Gly
277 65          70          75          80
279 acg ttt gaa gag aac ctt ggc aag acg gca ctc gac ttg gtg atg cag      288
280 Thr Phe Glu Glu Asn Leu Gly Lys Thr Ala Leu Asp Leu Val Met Gln
281          85          90          95
283 tcc aag gtg ttc cag gcg gtg ctt ccc cag agt gag gac tgc ctc acc      336
284 Ser Lys Val Phe Gln Ala Val Leu Pro Gln Ser Glu Asp Cys Leu Thr
285          100          105          110
287 atc aac gtg gtg ccg ccg ccg ggc acc aag gcg ggc gcc aac ctc ccg      384
288 Ile Asn Val Val Arg Pro Pro Gly Thr Lys Ala Gly Ala Asn Leu Pro
289          115          120          125
291 gtc atg ctc tgg atc ttt ggc ggt ggg ttt gag atc ggc agc ccc acc      432
292 Val Met Leu Trp Ile Phe Gly Gly Gly Phe Glu Ile Gly Ser Pro Thr
293          130          135          140
295 atc ttc cct ccc gcc cag atg gtc acc aag agt gtg ctc atg ggc aag      480
296 Ile Phe Pro Pro Ala Gln Met Val Thr Lys Ser Val Leu Met Gly Lys
297 145          150          155          160
299 cac atc atc cac gtg gcc gtc aac tac cgt gtt gcc tcg tgg ggg ttc      528
300 His Ile Ile His Val Ala Val Asn Tyr Arg Val Ala Ser Trp Gly Phe
301          165          170          175
303 ttg gct ggt gat gac atc aag gcc gag ggc agc ggg aac gcc ggc ttg      576

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VERIFICATION SUMMARY

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Input Set : A:\08919-066001.TXT

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